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Q07303 rattus norv

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                               3 homo sapien
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9 columba liv
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| oreochromis | Q91513 | PRLR_ORENI | 1 | 630 | 7.2 | 79 | G |
|-------------|--------|------------|----|------|-----|------|----|
| saccharomyc | | HXKA_YEAST | μ | 485 | 7.2 | 79 | 42 |
| homo sapien | P26992 | CNTR_HUMAN | _ | 372 | 7.2 | 79 | ω |
| sus scrofa | 018796 | IL6A_PIG | _ | 467 | 7.2 | 79.5 | N |
| caenorhabdi | Q18066 | DIM1_CAEEL | ب. | 323 | 7.2 | 79.5 | |
| mus musculu | P16872 | IL7R_MOUSE | _ | 459 | 7.3 | 80.5 | 0 |
| mus musculu | P26955 | CYRB_MOUSE | ب | 896 | 7.4 | 81 | 9 |
| phaseolus a | Q01390 | SUSY_PHAAU | _ | 805 | 7.5 | 82 | æ |
| homo sapien | P29317 | EPA2_HUMAN | _ | 976 | 7.6 | 83 | 7 |
| glycine max | P13708 | SUSY_SOYBN | _ | 805 | 7.6 | 83 | σ |
| mus musculu | Q62406 | IRA1_MOUSE | _ | 710 | 7.6 | 83 | 5 |
| homo sapien | P42702 | LIFR_HUMAN | 1 | 1097 | 7.6 | 83.5 | 4 |
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| X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244. X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244. MEDLINE=96291992; PubMed=8662530; Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S., Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.; "Functional mimicry of a protein hormone by a peptide agonist: the "Punctional mimicry of a protein hormone by a peptide agonist: the "Punctional mimicry of a protein hormone by a peptide agonist: the | SEQUENCE OF 1-17 FROM N.A. SEQUENCE OF 1-17 FROM N.A. MEDLINE=92147143; PubMed=1664413; Penny L.A., Forget B.G.; "Genomic organization of the human erythropoietin receptor gene."; Genomics 11:974-980(1991). [6] | SEQUENCE OF 1-96 FROM N.A. TISSUE-Placenta; MEDLINE-92399734; PubMed=1668607; MACOUCHE L., Tournamille C., Hattab C., Boffa G., Cartron J.P., Chretien S.; "Cloning of the gene encoding the human erythropoietin receptor."; Blood 78:2557-2563(1991). | SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Placenta; MEDLINE-9239733; PubMed-1668606; MEDLINE-92399733; PubMed-1668606; Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N., Hankins W.D.; "Cloning of the human erythropoietin receptor gene."; Blood 78:2548-2556(1991). | SEQUENCE FROM N.A. MEDLINE=91372359; pubMed=1654273; MEDLINE=91372359; pubMed=1654273; Ehrenman K., St John T.; "The erythropoietin receptor gene: cloning and identification of multiple transcripts in an erythroid cell line OCIMI."; Exp. Hematol. 19:973-977(1991). [2] EXP. Hematol. 19:973-977(1991). [2] EXP. HEMATOL. 19:973-977(1991). [2] MEDLINE=90304340; PubMed=2163696; MEDLINE=90304340; PubMed=2163696; Jones S.S., D'Andrea A., Haines L.L., Wong G.G.; "Human erythropoietin receptor: cloning, expression, and biologic characterization."; Blood 76:31-35(1990). | LTT 1 LHUMAN STANDARD; PRT; 508 AA. EPOR_HUMAN STANDARD; PRT; 508 AA. P19235; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Erythropoietin receptor precursor (EPO-R). EPOR. HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; |

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Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
Eggrie J., Stroud R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
PDB;
PDB;
PDB;
PDB;
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PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Efficiency of signalling through cytokine critically on receptor orientation."; Nature 395:511-516(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dimerization is not sufficient for activation. Nat. Struct. Biol. 5:993-1004(1998).
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "An antagonist peptide-EPO receptor complex suggests that receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jolliffe L.K., Wilson I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
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                                                                 1 KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL
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BL; M60459; AAA52403.1;

BL; S45332; AAB52371.1;

BL; M76595; AAA52393.1;

BL; M77244; AAA52392.1;

BL; M77244; AAA52392.1;

BL; M43799; A43799.

BL; A43924; A43924;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY & MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST
MECHANISM OF ERYTHROPOIETIN-INDUCED AND DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00060;
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18-NOV-98.
01-OCT-99.
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                                                                                                                                          Score 1060; DB 1;
Pred. No. 5.7e-96;
1; Mismatches 2;
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; F9F326E162E9512A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERYTHROPOIETIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
TYPE-III.
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01-FEB-1995
                                                                                                                                                                                                                                                  CHAIN
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
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Tabira T., Sasaki R.;
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01-FEB-1995
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HSSP; P19235;
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                                                                                                                                                                                                                                                                                                             Receptor;
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FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
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M., Takahata K.,
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STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-91080149; PubMed-2175360;
Kuramochi S., Ikawa Y., Todokoro K.;
"Characterization of murine erythropoietin receptor
"Characterization of murine erythropoietin receptor
J. Mol. Biol. 216:567-575(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Unregulated expression of the erythropoletin receptor gene caused insertion of spleen focus-forming virus long terminal repeat in a murine erythroleukemia cell line.";

MOI Cell min line in the more than the mor
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Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                           "Spleen focus-forming virus long terminal repeat activation of the murine erythropoietin receptor friend leukemia cell line.";
                                                                                                                                                                        MEDLINE=91201346; PubMed=1849897;
Lacombe C., Chretien S., Lemarchandel V.,
Gisselbrecht S., Cartron J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92017832; PubMed=1656233;
Hino M., Tojo A., Misawa Y., Mori
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                                      266:6952-6956(1991)
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Pred. No. 3.8e-78;
3; Mismatches 22;
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EMBL; M62360; AAA37582.1; -.
EMBL; S59388; AAB20029.2; -.
PIR; A32385; A32385.
PIR; A41686; A41686.
PIR; S13249; S13249.
                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
DISULFID
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a copyrend the swiss institute of Bioinformatics and the EMBL the European Bioinformatics institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miura O., Cleveland J.L., Thle J.N.;
"Inactivation of erythropoietin receptor function by point in a region having homology with other cytokine receptors. Mol. Cell. Biol. 13:1788-1795(1993).
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93180826; PubMed=8382775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION:
                       181
                                                  153
                                                                         121
                                                                                                   93
                                                                                                                          61
                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:95408; Epor.
                                                                                                                                                  KFESKAALLASRGSEELLCFTQRLEDLVCFWEEAASSGM-DFNYSFSYQLEGESRKSCSL
                                                                                                                                                               KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL
              TRITIAVRARMAEPSFGGFWSAWSEPVSLLT
                                                               RLADESGHVVIRWLPPPETPMTSHIRFELDISAGNGAGSVQRVELLEGRTECVLSNLRGR
                                                                                                             HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVA
                                                  RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
                                                                                                   HQAPTVRGSVRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVLLDAPAGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00041; fn3; 1.; SM00060; FN3; 1
                                                                                                                                                                                                   Similarity 77.7
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002996; CR1A.
IPR003961; FN_III.
                                                                                                                                                                                                                                                                                         25
250
250
273
147
52
90
                                                                                                                                                                                                                                                                                                                                                                                                                     HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                291
55194
                                                                                                                                                                                                                                                                                         507
249
272
507
212
62
106
                                                                                                                                                                                                               79.2%;
77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF THE STANDARD (POTENTIAL) (POTENTIAL)
W; 067657A2E26451CA CRC64;
                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                 ERYTHROPOIETIN RECEPTOR
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                            ≥ 869.5; DB 1;
. No. 2.3e-77;
                       211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                             AAB20029).
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        point
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                                                                                                                                                                                                                             507;
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RESULT 4
TPOR_MOUSE
                                                                                                     SOFT TO THE STREET AND THE RESERVE TO SOR CONTROL TO THE STREET AND THE STREET AN
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPOR_MOUSE
Q08351;
Q1-FEB-1995
Q1-FEB-1995
16-OCT-2001
                                                                                                DOMAIN
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93390934; PubMed-8397366; Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattei Souyri M., Cosman D., Gisselbrecht S.; "Characterization of the murine Mpl proto-oncogene, a memb hematopoietic cytokine receptor family: molecular cloning, chromosomal location and evidence for a function in cell goncogene 8:2607-2615(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPL OR TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily that transduces EMBO J. 12:2645-2653(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last annotation update)
Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97076; Mpl.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93327753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ICFW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Murine c-mpl: a member of the hematopoietic growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BL; Z22649; CAA80365.1;
BL; Z22657; CAA80372.1;
BL; X73677; CAA52031.1;
R; S35317; S35317;
SP; P19235; 1EBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A RE MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMURE RESPONSES. SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR TPOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.,
                                                                                                                                                                                                                                                                                                                                             PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (C-mpl).
                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                           26
483
505
117
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 31, Created)
(Rel. 31, Last sequence unit (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seldin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transduces a proliferative signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8334987;
n D.C., Chiang M.K.,
                                                                                                                                                                                                                                                                                                                HEMATOPO_REC_L_F1; 1.
mbrane; Glycoprotein; Signal; Repeat
                                                                                                                                           625
482
504
625
117
199
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Rodentia;
                                                                                                     69817
               15
24
             . 6%;
                                                                                                     Œ.
                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
MISSING (IN REF. 2).
             Score 171;
Pred. No. 4
                                                                                                                                                                                                                                                     THROMBOPOIETIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                   -> PVRTSPAGE (IN 309CF6EAA3724549
                                                                                                                                           -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            moved. usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peichel C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There a
             DB 1;
.9e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         its content
                                                                                                REF. 2)
CRC64;
                                                                                                                                                                                    · ·) (POTENTIAL)
                                 Length 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattei M.-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
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TPOR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE-92302297; PubMed-1608974; Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-Gisselbrecht S., Souyri M.; "Molecular cloning and characterization of MPL, the v-mpl oncogene: identification of a member of growth factor receptor superfamily."; Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Thrombopoietin receptor precursor (TPO-R) (
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and transcription of Genomics 20:5-12(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chretien S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mignotte V., Vigon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=94292186; PubMed=8020956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein) (C-MPL OR TPOR.
                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMURE RESPONSES.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; C-MPL-K (SHOWN HERE) AND C-MPL-P; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF CELLS OF HEMATOPOIETIC ORTGIN. THE TWO FORMS (C-MPL-K AND C-MPL-P) ARE ALWAYS FOUND TO BE COEXPRESSED.

DISBASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC THEOMORPHIC OF THE TWO FORMS.
                                                             SIMILARITY: CONTAINS 2 PIBRONECTIN TYPE III-LIKE DOMAINS. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIDATABASE: NAME-PROW; NOTE-CD guide CD110 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/11586825_g.htm".
                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                 THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO I
                                                                                                                                                                               ANOMALIES.
  SWISS-PROT en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPNPVPVLDQPPCVHPTASQPHGPAPFLTVKGGSCLVSGLQASKSYWLQLRSQPDGVSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSQPGELQIHWEAPAPE--ISDFLRHELRYGPTDSSNATAPSV--IQLLSTETCCPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVPTFGTRYVCQFPAQDEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVGLPAPPRVIKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA - - PSGTYQLLYAYRGEKPRACPLYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTARGAIRFWCSLPTAD-TSSFVPLELRLTAAS-GAPRFHRVIHINEVVLLDAPVGLVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (C-mpl) (CD110 antigen).
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                      entry is
                                                                                                                                 BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN
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copyright. It is produced through tute of Bioinformatics and the EN
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Catarrhini; Hominidae
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Matches 59
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EMBL; M90103; AAA69972.1; -
EMBL; U68162; AAB08424.1; -
EMBL; U68159; AAB08424.1; -J
EMBL; U68161; AA5266; A45266.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                        MAEPSFGGFWSAWSEPVSL 209
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  PDGISLGGSWGSWSLPVTV
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IPR003528;
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CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

RIKHALWEDLEDLHAVLGQUIADTAALSPEKATVSDTCEEV

EPSLLEILPKSSERTP -> YRDRQAGDWRWTRWSRTCKQA

FLVRSYTEPLARPPPVRTYGFALPARHLWDSPRLLTL (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 146;
Pred. No. 1
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A -> V (IN DBSNP:6087).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_011989
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RESULT 6

PRILR_BOVIN

ID

PRILR_BOVIN

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O28172;
D7

O1.NOV-1997 (Rel. 35, Created)
D7

O1.NOV-1997 (Rel. 35, Last sequence update)
D7

O1.NOV-1997 (Rel. 35, Last sequence update)
D7

O1.NOV-1997 (Rel. 36, Last annotation update)
D7

O1.NOV-1997 (Rel. 36, Last annotation update)
D8

PRILR.
OS

B0s taurus (Bovine)
OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebra;
OC

Bowidae; Bovinae; Bos.
OC

Bowidae; Bovinae; Bos.
OC

Bovidae; Bovinae; Bos.
OC

ROBL_TAXID-9913;
RN

[1]
RP

SCOUTE PROM NA., Schuler L.A.;

"Molecular cloning of the bovine prolactin receptor transcrivation."
RY

Mol. Cell. Endocrinol. 89:47-58(1992).
CC

-i-SUBCLELLUAR LOCATION: Type I membrane proteing for prolacental tissues.";
RI

MOL. Cell. Endocrinol. 89:47-58(1992).
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-i-SUBCLELLUAR LOCATION: Type I membrane proteing for prolacental tissues.
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MEDLINE=93246019; PubMed=1338725;
Scott P., Kessler M.A., Schuler L.A.;
Scott Power cloning of the bovine prolactin receptor and Molecular cloning of the bovine prolacting transcripts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues; ; mol. Cell. Endocrinol. 89:47-58(1992).
-i- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
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                                                         63 APTARGAIRFWCSLPTADTSSFVPLELRLTA-----ASGAPRFHRVIHINEVVLLDAPV 116
                                                                                                                          20
                                                                                                                                                                                7 ALLAARGPEE----LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA
                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                             10.7%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal; Repeat.
POTENTIAL.
                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIA)
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                             Pred. No. 0.0(
0; Mismatches
                                                                                                                                                                                                                                                                             Score 118; DB 1;
Pred. No. 0.00068;
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
; 7385C0D6956EE139 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                101;
                                                                                                                                                                                                                                                                                                          Length 581
                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        distribution fetal and
                                                                                                                                                                                                                                                30;
                                                                                                                          TLIHE.
                                                                                                                                                                                                                                             Gaps
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                       Query Match
Best Local
     Matches
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01-NOV-1997 (Re
01-NOV-1997 (Re
Growth hormone
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CARBOHYD
CARBOHYD
                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                  DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P10912; 1HWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein).
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                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLVARL---ADESGHVVIRWLPPPETPMTSH---IRFELDISAGNGAGSVQRVELLEGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECVLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X70041; CAA49635.1;
       35;
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                             PS01352;
                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, (Rel. 35, Rel. 35, Rel. 35,
                                                                                                                                                                                                                                                                    19
19
261
285
141
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       Conservative
                                                                                                            56
97
122
46
73
111
152
157
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                                                                                                                                                                                                                                                                                                                                                                                             HEMATOPO_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos.
                                                                                                                            634
260
284
634
248
248
108
108
136
136
136
131
111
152
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Cetartiodactyla; Ruminantia; Pecora;
                                                                                            70979
                       10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
or precursor (GH recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                       PO_REC_L_F1; 1.
Glycoprotein; Signal.
                                                                                            MW;
                                                                                     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF SIMILARITY.

OF SIMILARITY.

OF SIMILARITY.

OF SIMILARITY.

OF SIMILARID (GLCNAC...) (PO SIMIRED (GLCNAC...)) (PO SIMIRED (GLCNAC...) (PO SIMIRED (GLCNAC...)) (PO SI
       25;
     Score 112.5;
Pred. No. 0.00
25; Mismatches
                                                                                                                                                                                                                                                                                                                     GROWTH HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
receptor)
. 0.0026;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
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                                                                                            CRC64;
                                       Length
         Indels
                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding
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                                         634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovoidea;
       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in no way
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RESULT 8
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                                                                                                                                     entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-9 receptor procure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92307307; PubMed-1376929; Renauld J.C., Druez C., Kermouni a van Roost E., van Snick T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL9R_HUMAN
Q01113; Q14634;
Q1-APR-1993 (Re
                                                                                                                                                                                                                                                                                                                                                                            "The II-9 receptor gene (IL9R): genomic structure, chrolocalization in the pseudoautosomal region of the long chromosomes, and identification of IL9R pseudogenes at 16pter, and 18pter.";
Genomics 29:371-382(1995).
-!- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND STREET OF THE PROTEIN AND STREET OF 
                                       EMBL;
EMBL;
EMBL;
                                                                                                                                                   use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement (S)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96115587; PubMed=8666384;
Kermouni A., van Roost E., Arden K.C., Verme
Godelaine D., Flint J., Lurquin C., Szikora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-94250901; PubMed-8193355;
Chang M.S., Engel G., Benedict C.,
"Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godelaine D., Flint J., Lurquin Marynen P., Renauld J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-9 receptor precursor (IL (IL9RX OR IL9R) AND (IL9RY OR IL9R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood 83:3199-3205(1994).
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                                       , M84747; AAA58679.1;
, S71404; AAB30844.2;
, S71420; AAD14081.1;
, L39064; AAC29513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADILVKWEPPPNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                               HIS IS A RECEPTOR FOR INTERLEUKIN-9.
LOCATION: TYPE I MEMBRANE PROTEIN AND SECRET BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                         institutions as long
                                                                                    ALT_SEQ
                                                                                                                                                                                                 is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89:5690-5694(1992)
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(IL-9R).
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the human interleukin-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522
                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vermeesch J.R., Weiss
ikora J.P., Higgs D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋛
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                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                      its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosomal
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                                                                                                                                                                                                                                                                                                                                                                                   SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arm of the sex
9qter, 10pter,
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B45268

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RESULT 9
GHR_SHED
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                            GHR_SHEEP JIANUAL GHR_SHEEP Q28575;
Q28575;
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                 CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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GHR.
                                                                                                                                                                                                                                                   MEDLINE=91099608;
                                                                                                                                                                                                                                                                                                                                                  Bovidae;
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                                   between
                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                  European Bioinformatics Institute.
           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGLVARLADESGHVVIRW-LPPPETPMTSHIRFELDISAGNGA-GSVQRVELLEGRTECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGPRSRTFTCLTNNILRIDCHW-SAPELGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGPEE---LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEAFELDPGFIHEARLRVQMATLEDDVVEEERYTGQWSEWSQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----CILRGSECTVVLPPEAVLVPSDNFTITFHHCMSGREQVSLVDPEYLPRRHVKLDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRFWCSLPTADTSSFVPLELRLTAASG-APRFHRVIHINEV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                              Caprinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01355;
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IPR003531; Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
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292
150
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440
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                                                                                                                                                                                                                                                       PubMed=1980117;
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                                                                                                                                                                                                                                                                                                                                                Ovis
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522
270
291
291
522
522
244
439
443
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                                                                                                                                                                                                                                                                                                                                                               Cetartiodactyla; Ruminantia;
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23
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N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
R-> G (IN REF. 3).

MISSING (IN REF. 3).
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Pred.
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CYTOPLASMIC (
FIBRONECTIN T
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-9 RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E6CB5C6342DE2BB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
as long
                                                                                                                                                                                                    Brandon M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111;
No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
.0029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 522;
                                                                                                                                                                                                                                                                                                                                                               Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
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                                                                                                                                                                                                               ontogeny
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                                                                                                                                                              HORMONE
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DT 01-NOV
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DE PROLAC
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OS CETVUS
OC EUKARY
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Best Local
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                    Clarke L.A., Edery M., Loudon A.S., Randuck.
Kelly P.A., Jabbour H.N.;
"Expression of the prolactin receptor gene during t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                  non-breeding seasons in red deer (Cervus expression of two forms in the testis."; J. Endocrinol. 146:313-321(1995).
                                                                                                                                                                                                                                                                                                                                       Q28235;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                       MEDLINE=96030711; PubMed=7561644;
                                                                                                                                                                                                                                      Cervidae;
                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                            Cervus elaphus (Red
                                                                                                                                                                                                                                                                                                                                 Prolactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M82912; AAA73171.1; -. HSSP; P10912; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=9860;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRLR_CEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed
                                                                                                                                                         IISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRSPELETFSCHWTDGANHSLQSPGSVQMFYIRRDIQEWKEC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFTERLEDLVCFFEEAASAGV-GPGNFS-FSFQLEDEPWKLCRLHQAPTARGAIRFWCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00041; fn3; 1.
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IPR003961; FN_III.
                                                                                                                                                                                                                                                      Eutheria;
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                                                                                                                                                                                                                                    Cervinae;
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19
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196
70844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEMATOPO_REC_L_F1; 1
                                                                                                                                                                                                                                                                                                                                 precursor (PRL-R).
                                                                                                                                                                                                                                      Cervus
                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Cervoide
                                                                                                                                                                                                                                                                                          deer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%;
26.6%;
    A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110.5;
Pred. No. 0.00
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

CYTOPLASMIC (POTENTIA FIBRONECTIN TYPE-III. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC. N-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 0.0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                      Pecora; Cervoidea;
                                                          the breeding a evidence for
                                                                                                                   Postel-Vinay M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                              and
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                                                                                                                                                                                                                                                                                             GHR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                   GHR_CHICK Q02092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
Growth hormone receptor precursor (GH recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                     protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
NCBI_TaxID=9031;
                                          Archosauria; Aves;
                                                                   Eukaryota;
                                                                                      Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01352; HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                182 RITIAVRARMAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 PKIIKCRSPGKETFTCWWEPGSDGGL-PTNYTLTYHKEGE----TLIHECPDYKTGGPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGAIRFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROLACTIN.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYFSKKHTSIWKIYVITVNAINQMGVSSSDPLY---VDVTYIVEPEPPANLTLELKHPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSLPTADTSSFVPLELRLTA-----ASGAPREHRVIHINEVVLLDAPVGLVARL---AD
                                                                                                                                                                                                                                                                                                                                                                                         KYLVQVRCK---PDH-GYWSEWSPESSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETAAD--WEIHFAAKQTQLKIFSLYPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGHVVIRWLPPPETPMTS----HIRFELDISAGNGAGSVQRVELLEGRTECVLSNLRGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X94953; CAA64419.1;
P14787; LAN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 9.8%;
l Similarity 20.7%;
43; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002996; CR1A.
IPR003961; FN_III.
IPR003528; Hematop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 AA;
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581
234
258
581
122
227
26
86
86
59
                                       Neognathae;
                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal; Repeat.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type I membrane protein.

THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

BY SIMILARITY.

BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 108; DB 1;
Pred. No. 0.0064;
1; Mismatches 9
                                       Craniata; Vertebrata; Euteleostom1;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                        update)
receptor)
                                                                                                                                                                                                                                                                        809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 581;
                                                                                                                                                        (Serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
                                                                                                                                                        binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91243665; PubMed-2036984;
Burnside J., Liou S.S., Cogburn L.A.;
Molecular cloning of the chicken growth hormone receptor
complementary deoxyribonucleic acid: mutation of the gene
sex-linked dwarf chickens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: BROAD SPECIFICITY.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S32823; S32823.
HSSP; P10912; 1HWH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M74057; AAA48781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 128:3183-3192(1991).
-i- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                            179
                                                                                      137
                                                                                                                                127
193 MGRDYEIRVRSRQRTSEKFGEF
                                                                                                                                                                          78
                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                    14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQL----EDEPWKLCRLHQAPTARG
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                          GRTRITIAVRARM-AEPSFGGF
                                                                                      GIHGDIQVRWDPPPTADVQKGWITLEYELQYKEVNET---
                                                                                                                              ---GHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTECV--LSNLR 178
                                                                                                                                                                        AGENSCYFNTSYTSIWIPYCVKL-ANKDEVFDEKCFSVDEIVLPDPPVHLNWTLLNTSQT
                                                                                                                                                                                                                    AIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES--
                                                                                                                                                                                                                                                              PQISKCRSPELETFSCYWTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01352; HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
238
262
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117
72
72
97
127
132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FN3;
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237
261
608
608
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171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. .) (POT N
                                            199
                                                                                                                                                                                                                                                                                                                                                                    Score 107;
Pred. No. 0.
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InterPro; IPR003961; FN_III.
InterPro; IPR0039528; Hematopo_receptor_L_F1.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Smarr; Sm00041; fn3; 1.
Smarr; Sm00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- EUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCILIULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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             Similarity 26.;
53; Conservative
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tazoa; Chordata; Cr
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                          CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
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-!- FUNCTION: THIS IS A RECEPTOR
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Halaby D., Thoreau E., Djiane J., Mornon J.P.;
"Homology modeling of rabbit prolactin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata; Craniata;
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
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MEDLINE=89184578; PubMed=2928321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 titles requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A30304; A30304.
1AN3; 03-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J04510; AAA31457.1;
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                                                                                                                                                                                                                                                                                                                                                                                                          PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002996; CR1A.
IPR003961; FN_III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor precursor (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003528;
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     FN3;
                                                                                                                                                                                                                                                                                                                                                                                                    HEMATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 30-228
                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Sig
BY SIMILARITY
  W.
                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIA)
FIBRONECTIN TYPE-III |
FIBRONECTIN TYPE-III |
BY SIMILARITY
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                          N-LINKED
                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86:2112-2116(1989).
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  800E3166FEF7108C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR THE ANTERIOR
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                          update)
                                                                                                                                                                                                                                                                                                                                                                         Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complexed
     CRC64;
                                                                                                                                                                       2.
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                             (POTENTIAL)
                                                        (POTENTIAL)
                                                                                   (POTENTIAL).
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DT 01-AU
DT 01-MA
DE GROWT
DE GHR.
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RM [2]
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHR_MOUSE STANDARD; PKI; UP16882; P16590; Q9R264;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Growth hormone receptor precursor (GH
REVISIONS.
STRAIN-C57BL;
                                    hormone receptor gene.";
Receptor 4:223-227(1994)
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse serum growth hormone (GH) binding proextracellular and substituted transmembrane Mol. Endocrinol. 3:984-990(1989).
                                                                                                                                                                SEQUENCE OF 156-650
                                                                                                                                                                                                                                                                            STRAIN=Swiss Webster, and DBA/2J; MEDLINE=95080157; PubMed=7988474;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Swiss Webster, and DBA/2J;
MEDLINE=99367316; PubMed=10425445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE=89295449; PubMed=2739661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                 MEDLINE=95201642;
                                                                                                                                                                                              Endocrinology 135:2802-2805(1994).
                                                                                                                                                                                                               splicing.";
                                                                                                                                                                                                                              receptor transcripts
                                                                                                                                                                                                                                                            Edens A., Southard J.N., Talamantes F.;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                          Moffat J.G., Edens A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith W.C., Kuniyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                        hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GHBP)
                                                                                                                                                                                                                                           Mouse growth
                                                                                                                                                                                                                                                                                                                                                                         "Structure and expression of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KILSLYPGQKYLVQVRCK---PDH-GFWSVWSPESSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLEVKHPEDRKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAA--EWETHFAGQQTQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VARLADESGHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYKTGGPNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRY---VDVTYIVEPDPPVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TARGAIRFWCSLPTADTSSFVPLELRLTAAS-----GAPREHRVIHINEVVLLDAPVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPFIFKCRSPEK-----ETFTCWWRPGADGGL-PTNYTLTYHKEGE----TITHECP
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                                                                                 n encoding the mouse terminus is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                          binding protein gene.";
Endocrinol. 23:33-44(1999).
                                                                                                                He L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                             hormone
                                                                                                                  Kopchick J.J
                                                                                                                                 PubMed=7894338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 9.5%;
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                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                              are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.,
                                                                                                                                                                                                                            receptor/binding are produced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein).
                                                                                                                                                                                                                                                                                                                                                                                          Talamantes F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Talamantes F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                 growth hormone between exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                               (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
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receptor)
                                                                                                                                                                                                                              protein
a single
                                                                                                                                                                                                                                                                                                                                                                         growth hormone receptor/growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein has G
ane domains.";
                                                                                                                                                                                                                              single
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                                                                                 binding protein (mGHBP) and 8 of the mouse grow
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                                                                                                                                                                                                                            and growth
gene by al
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GH
                                                                                                                                                                                                                              th hormone alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein)
                                                                                 growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
      EMBL; U49266; AAK62802.1; EMBL; U49268; AAK62802.1; EMBL; U49268 AAK62802.1; EMBL; U43933; AAK62802.1; HSSP; P10912; 1HWH. MGD; MGI:95708; Ghr.
                                                                                                                                                                                                                                                                           InterPro; IPR002996; (InterPro; IPR003961; InterPro; IPR003528; InterPro; IPR003528; InterPro; IPR0041; In3; 1
                                                 CARBOHYD
CARBOHYD
                                                                                                DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
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EMBL;
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modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                  CARBOHYD
                                                                                                                                                                                                                CHAIN
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith W.C., Colosi P., Talamantes F.; "Isolation of two molecular weight variants
                                                                                                                                                               DOMAIN
                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-41.
MEDLINE=88288223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou Y., He L., Kopchick J.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                             PRÓSITE; PS01352; HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTETED (1SOFORM 2):
ALTERNATIVE PRODUCTS: 2 isoforms; 1/HMW GHR (shown here)
GHR; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      concentration of gh. SUBUNIT: ISOform 1 is SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    may play an important role in regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF120488;
AF120487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF120481;
AF120482;
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AF120486;
AF120487;
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AF120484;
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AF120482;
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M31680; AAA37689.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         AF120486;
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                                                                                                                                                                                                                                           Transmembrane;
                     25
274
274
298
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AAD32555.1;
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AAD32556.1;
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FN_III.
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                                                                                                                                                                                                                                             Glycoprotein; Signal; Alternative
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CYTOPLASMIC
FIBRONECTIN
                                                                                                BY SIMILARITY.
BY SIMILARITY.
                N-LINKED (GLCNAC. ...) (POTENTIAL).
DIOFPWFLLIIFGIFGVAVMLEVVIF -> GTKSNSQHPHO
                                                                                                                                                                                                                GROWTH HORMONE RECEPTOR
                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                 TYPE-III.
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Matches 51
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Q04594;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Prolactin receptor precursor (PRL-R) (CPRLP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-WHITE LEGHORN; TISSUE-Kidney;

MEDLINE-93075121; PubMed-1445292;

Tanaka M., Maeda K., Okubo T., Nakashima K.;

Tanaka M., Maeda K., Okubo T., Nakashima K.;

"Double antenna structure of chicken prolactin receptor
"Double antenna structure of chicken prolactin receptor
the cDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _CHICK
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                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                          PROLACTIN.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 188:490-496(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                         EMBL; D13154; BAA02439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110
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                                                                                                                      JQ1655; JQ1655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLADES - - - - - GHVVIRWLPPPETP-MTSHIRFELDISAGNGAGSVQRVELLEGR - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PDYVSAGKNSCYFNSSYTSIWIPYCIKLT-TNGDLLDQKCFTVDEIVQPDPPIGLN
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T -> A (IN REF. 6).
G -> A (IN REF. 3 AND 4).
E -> G (IN REF. 2).
R -> A (IN REF. 2).
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Pred. No. 0.02;
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G -> A (IN REF. 3 AND 4).
E -> G (IN REF. 2).
R -> A (IN REF. 2).
95653380CAF0B931 CRC64;
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(CPRLP).
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                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
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397
                                   337
                                                                       280
                                                                                                           233
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                                                                                                                          5 KAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAP
                                                                    DYRTAGPNSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHY---VDVTYIVQPDPPVNV
                                                                                        TARGAIRFWCSLPTADTSSFVPLELRLTAA-----SGAPRFHRVIHINEVVLLDAPVGL
FSLNPGKKYIIQIHCK --- PDHHGSWSEWS
                 SNLRGRTRITIAVRARMAEPSFGGFWSAWS
                                  TLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQQTQYKM
                                                   VARL----ADESGHVVIRWLPPPETPMTS-HIRFELDISAGNGAGSVQRVELLEGRTECVL
                                                                                                         KPTIIKCRSPEK-----ETFTCWWKPGLDGG-HPTNYTLLYSKEGEE-----QVYECP
                                                                                                                                              42;
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326
36
75
79
100
112
132
262
303
315
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                             HEMATOPO_REC_L_F1;
                                                                                                                                                                                                    9.4%;
                                                                                                                                                                                           94102
                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal; Repeat
                                                                                                                                                                                          MΨ;
                                                                                                                                             37;
                                                                                                                                             Score 103.5;
Pred. No. 0.02
37; Mismatches
                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC
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                                                                                                                                             102;
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                                                                                                                                              Indels
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                                                                                                                                                              831;
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                                                    174
                                                                                        118
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Search completed: August 28, 2002, 17:40:42 Job time: 533 sec